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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:33 ; Search time 11 seconds
(without alignments)
20.462 Million cell updates/sec

Title: US-09-648-816B-9
Perfect score: 69
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	36	52.2	255	9	US-09-989-293A-287
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22	36	52.2	371	9	US-09-792-356-12	Sequence 12, Appl
23	36	52.2	371	10	US-09-899-422-12	Sequence 2, Appl
24	36	52.2	455	9	US-09-898-234-2	Sequence 2, Appl
25	36	52.2	455	9	US-09-898-234-17	Sequence 17, Appl
26	36	52.2	455	9	US-09-756-854-5	Sequence 5, Appl
27	36	52.2	455	9	US-09-899-429A-2	Sequence 2, Appl
28	36	52.2	455	9	US-09-899-429A-27	Sequence 27, Appl
29	36	52.2	455	9	US-10-041-574-5	Sequence 5, Appl
30	36	52.2	455	9	US-09-792-356-2	Sequence 2, Appl
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42	36	52.2	455	12	US-10-120-397-2	Sequence 2, Appl
43	36	52.2	469	9	US-09-992-598-289	Sequence 289, App
44	36	52.2	469	9	US-09-989-293A-289	Sequence 289, App
45	36	52.2	469	9	US-10-063-547-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-864-761-48620
Sequence 48620, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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US-09-822-263-14
; Sequence 14, Application US/09822263
; Patent No. US20020036598A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Verneil, Corine
; APPLICANT: Shimkets, Richard A
; APPLICANT: Burgett, Catherine
; APPLICANT: Splet, Kimberly
; APPLICANT: Tcherev, Velizar T
; TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and polypeptides Encoded TH
; FILE REFERENCE: 15966-572 CIP1
; CURRENT APPLICATION NUMBER: US/09/822,263
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/672,665
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; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
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Best Local Similarity 71.4% Pred. No. 1e+02;
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Db 42 YKKWENE 48

RESULT 4

US-09-989-293A-287
; Sequence 287; Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Gunney, Austin L.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 9; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKMKK 9
|||||:
Db 42 YKKWENE 48

RESULT 5
US-09-989-735-287

;; Sequence 287, Application US/09989735
;; Publication No. US20020193295A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Bolstein, David

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerlisen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: p2730p1c61
;; CURRENT APPLICATION NUMBER: US/09/989,735
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 9; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKNK 9
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Db 42 YKKWENE 48

RESULT 6
US-09-990-444-287
Sequence 287, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Geiber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.

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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1c19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 9; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 YKKWNRK 9
| | | | |
Db 42 YKKWENE 48

RESULT 7
US-09-989-722-287
Sequence 287, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730163
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 42 YKKWENE 48

RESULT 8
US-09-989-723-287
Sequence 287, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P162
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19

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PRIOR APPLICATION NUMBER: 60/062250	PRIOR FILING DATE: 1997-10-17
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Query Match      52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      42 YKKWKNK 48

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Sequence 287, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
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PRIOR FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-07-09

Query Match 52.2% Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0

QY 3 YKKMKR 9
Db 42 YKKMNE 48

RESULT 10
US-09-989-727-287
Sequence 287, Application US/0989727
Patent No. US20020072497A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC65
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,727
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 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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 Db 42 YKKWENE 48

RESULT 11
 US-09-989-731-287
 Sequence 287, Application US/09989731
 Patent No. US20020103125A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Goddard, Audrey E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhong, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C70
 CURRENT APPLICATION NUMBER: US/09/989,731
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/078910
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Best Local Similarity 71.4% Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 287; Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 42 YKKWENE 48

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RESULT 13

US-09-991-073-287

Sequence 287, Application US/09991073

Patent No. US20020127576A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Geider, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC15

CURRENT APPLICATION NUMBER: US/09/991,073

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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Query Match 52.2%; Score 36; DB 10; Length 255;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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PRIOR FILING DATE: 1998-07-09

Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fond, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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Query Match 52.2%; Score 36; DB 10; Length 255;

Best Local Similarity 71.4%; Pred. No. 1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:08 : Search time 35 Seconds

(without alignments)
49,493 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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6	53	76.8	19	20	AAV57501
7	53	76.8	20	20	AAV57502
8	53	76.8	25	20	AAV57496
9	53	76.8	35	20	AAV57497
10	49	71.0	18	20	AAV57500

11	49	71.0	18	20	AAV57504
12	48	69.6	13	20	AAV57468
13	48	69.6	14	20	AAV57467
14	47	68.1	13	20	AAV57466
15	47	68.1	18	20	AAV57503
16	44	63.8	798	21	AAV57501
17	44	63.8	925	21	AAV57502
18	44	63.8	1002	21	AAV57500
19	43	62.3	18	12	AAV57497
20	43	62.3	18	12	AAV57499
21	43	62.3	18	12	AAV57501
22	43	62.3	18	12	AAV57502
23	43	62.3	19	21	AAV57496
24	43	62.3	19	21	AAV57497
25	42	60.9	13	20	AAV57469
26	42	60.9	60	22	AAV57508
27	42	60.9	132	23	AAV57509
28	42	60.9	1971	21	AAV57500
29	42	60.9	1971	22	AAV57501
30	42	60.9	1971	22	AAV57502
31	41	59.4	213	23	AAV57503
32	41	59.4	314	18	AAV57504
33	41	59.4	314	23	AAV57505
34	41	59.4	356	23	AAV57506
35	41	59.4	398	18	AAV57507
36	41	59.4	398	23	AAV57508
37	41	59.4	415	22	AAV57509
38	40	58.0	18	20	AAV57510
39	40	58.0	127	20	AAV57511
40	39	56.5	18	12	AAV57512
41	39	56.5	18	12	AAV57513
42	39	56.5	18	12	AAV57514
43	39	56.5	20	12	AAV57515
44	39	56.5	23	12	AAV57516
45	39	56.5	115	18	AAV57517

ALIGNMENTS

```

RESULT 1
ID AAV57471 standard; Peptide: 13 AA.
AC AAV57471;
XX
XX
XX 25-FEB-2000 (first entry)
DE Antimicrobial peptide RP-7 SEQ ID NO:9.
XX
XX Antimicrobial; metaprotein; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX
XX Synthetic.
OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US03350.
XX
XX 18-FEB-1998; 98US-0025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX
XX WPI: 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi
XX

```

Antimicrobial pept
Antimicrobial pept
Antimicrobial pept
Antimicrobial pept
Antimicrobial pept
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Cationic oligopept
Antibacterial pept
Antibacterial pept
Antibacterial pept
Antibacterial pept
Antibacterial pept
Human polyprotein
Streptococcus poly
Mouse GAMP protein
Murine CALP relat
Murine SHD1 relat
D. Immitis cystein
D. Immitis cystein
D. Immitis cystein
D. Immitis cystein
CLASP-3 protein fr
Antimicrobial pept
Fragment of human
Cationic oligopept
Cationic oligopept
Cationic oligopept
Cationic oligopept
Cationic oligopept
S. pneumoniae cell

PS Disclosure: Page 110; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXXB, BXZXXB, XBBXXBBX, and
 CC XBBXXBBXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid. The peptides can be used to treat bacterial and
 CC more other amino acids. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 13 AA;

Query Match 100.0%; Score 69; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLKLS 13
 |||||

Db 1 ALYKKWKNKLKLS 13

RESULT 2
 AAY57472
 ID AAY57472 standard; Peptide; 18 AA.

XX AAY57472:
 AC 25-FEB-2000 (first entry)
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-8 SEQ ID NO:10.
 XX
 DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 OS
 XX WO9942119-A1.
 PN 26-AUG-1999.
 PD 17-FEB-1999; 99WO-US03350.
 PF 18-FEB-1998; 98US-0025319.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI: 1999-527417/44.
 DR WPI: 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 PS Disclosure: Page 111; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXXB, BXZXXB, XBBXXBBX, and
 CC the group consisting of XBBXXB, XBBXXBBX, BXZXXB, XBBXXBBXZ, and

CC XBBXXBBXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 18 AA;

Query Match 81.2%; Score 56; DB 20; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.068;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKWKNKLKRS 13
 |||||

Db 2 LYKKWKNKLKRS 13

RESULT 3
 AAY57470
 ID AAY57470 standard; Peptide; 14 AA.

XX AAY57470:
 AC 25-FEB-2000 (first entry)
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-6 SEQ ID NO:8.
 XX
 DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 OS
 XX WO9942119-A1.
 PN 26-AUG-1999.
 PD 17-FEB-1999; 99WO-US03350.
 PF 18-FEB-1998; 98US-0025319.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI: 1999-527417/44.
 DR WPI: 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 PS Disclosure: Page 109; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBXXBBX and BXXZBXXZ; and
 CC (b) a second peptide template XBBXXB, BXZXXB, XBBXXBBX, and
 CC the group consisting of XBBXXB, XBBXXBBX, BXZXXB, XBBXXBBXZ, and
 CC XBBXXBBXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

SO Sequence 14 AA;

Query Match 79.7%; Score 55; DB 20; Length 14;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKMKKLLK 12
 ||||| ||||
 DB 2 LYKKMKKLLK 12

RESULT 4

AAV57465
 ID AAV57465 standard; Peptide: 18 AA.

XX AAV57465;

DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide RP-1 SEQ ID NO:3.

XX Antimicrobial; metapetide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO942119-A1.

PD 26-AUG-1999.

XX 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -

PS Claim 17; Page 106; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBXXB and BXXZBXXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXB, XBBXXB, BXZXXB, XBBXXB, and
 CC XBBXXBXXZBXX, where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 18 AA:

Query Match 76.8%; Score 53; DB 20; Length 18;

Best Local Similarity 84.6%; Pred. No. 0.19;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKMKKLLKS 13
 |||||:| |||||
 DB 1 ALYKKMKKLLKS 13

RESULT 5
 AAV57499
 ID AAV57499 standard; Peptide: 19 AA.

XX AAV57499;

DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.

XX Antimicrobial; metapetide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO942119-A1.

PD 26-AUG-1999.

XX 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI: 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -

PS Disclosure: Page 58; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBXXB and BXXZBXXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXB, XBBXXB, BXZXXB, XBBXXB, and
 CC XBBXXBXXZBXX, where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 19 AA:

Query Match 76.8%; Score 53; DB 20; Length 19;

Best Local Similarity 84.6%; Pred. No. 0.2;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKMKKLLKS 13
 |||||:| |||||
 DB 2 ALYKKMKKLLKS 14

RESULT 6

AAV57501
 ID AAV57501 standard; Peptide: 19 AA.

XX AAV57501;

DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.

KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
XX Oryctolagus cuniculus.
XX
PN WO9942119-A1.
PD
XX 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi -
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
activity or for potentiating antimicrobial agents active against
organisms such as bacteria and fungi. The AP comprises: (a) a peptide
containing an amino acid sequence selected from the group consisting
essentially of a first peptide template XZBZXBXB and its derivatives
selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBZXBXZ; and
(b) a second peptide template XBBXX and their derivatives selected from
XBBZXBBXZBBX; where B = at least one positively charged amino acid;
X = at least one non-polar hydrophobic amino acid; Z = at least one
aromatic amino acid, and where B, X and Z may be separated by one or
more other amino acids. The peptides can be used to treat bacterial and
fungal infections. The peptides also increase the antimicrobial activity
of neutrophils. The peptides overall effect cellular disruption and
rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
sequences used in the exemplification of the present invention.
XX
CC
XX
SQ Sequence 19 AA;
Query Match 76.8%; Score 53; DB 20; Length 19;
Best Local Similarity 84.6%; Pred. No. 0.2;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALYKKMKKLKLS 13
DB 1 ALYKKMKKLKLS 13
RESULT 7
AAY57502
ID AAY57502 standard; Peptide; 20 AA.
XX
AC AAY57502;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
XX Oryctolagus cuniculus.
XX
PN WO9942119-A1.
PD 26-AUG-1999.
XX

PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi -
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
activity or for potentiating antimicrobial agents active against
organisms such as bacteria and fungi. The AP comprises: (a) a peptide
containing an amino acid sequence selected from the group consisting
essentially of a first peptide template XZBZXBXB and its derivatives
selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBZXBXZ; and
(b) a second peptide template XBBXX and their derivatives selected from
XBBZXBBXZBBX; where B = at least one positively charged amino acid;
X = at least one non-polar hydrophobic amino acid; Z = at least one
aromatic amino acid, and where B, X and Z may be separated by one or
more other amino acids. The peptides can be used to treat bacterial and
fungal infections. The peptides also increase the antimicrobial activity
of neutrophils. The peptides overall effect cellular disruption and
rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
sequences used in the exemplification of the present invention.
XX
CC
XX
SQ Sequence 20 AA;
Query Match 76.8%; Score 53; DB 20; Length 20;
Best Local Similarity 84.6%; Pred. No. 0.21;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALYKKMKKLKLS 13
DB 2 ALYKKMKKLKLS 14
RESULT 8
AAY57496
ID AAY57496 standard; Peptide; 25 AA.
XX
AC AAY57496;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
XX Oryctolagus cuniculus.
XX
PN WO9942119-A1.
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX

PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi -
PS Disclosure: Page 126; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXB, BXZXB, BXZXZXB, XBZXZBXB and BXZBXBXZ; and
CC (b) a second peptide template XBZBXBXB and their derivatives selected from
CC the group consisting of XBZBXBX, XBZBXBXB, BXZBXBXB, and
CC XBZBXBXBXZBXB; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 25 AA:
Query Match 76.8%; Score 53; DB 20; Length 25;
Best Local Similarity 84.6%; Pred. No. 0.27;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKKMKKILKS 13
1 ALYKKMKKILKS 13
Db 1 ALYKKMKKILKS 13
RESULT 9
AAY57497
ID AAY57497 standard; Peptide: 35 AA.
XX
AC AAY57497;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
XX
KM Antimicrobial: metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI: 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi -
PS Disclosure: Page 126; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXB, BXZXB, BXZXZXB, XBZXZBXB and BXZBXBXZ; and
CC (b) a second peptide template XBZBXBXB and their derivatives selected from
CC the group consisting of XBZBXBX, XBZBXBXB, BXZBXBXB, and
CC XBZBXBXBXZBXB; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.

CC selected from XBZBXBXBXB, BXZXB, BXZXZXB, XBZXZBXB and BXZBXBXZ; and
CC (b) a second peptide template XBZBXBXB and their derivatives selected from
CC the group consisting of XBZBXBX, XBZBXBXB, BXZBXBXB, and
CC XBZBXBXBXZBXB; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 35 AA:
Query Match 76.8%; Score 53; DB 20; Length 35;
Best Local Similarity 84.6%; Pred. No. 0.37;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKKMKKILKS 13
1 ALYKKMKKILKS 13
Db 1 ALYKKMKKILKS 13
RESULT 10
AAY57500
ID AAY57500 standard; Peptide: 18 AA.
XX
AC AAY57500;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
XX
KM Antimicrobial: metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US03350.
XX
PR 18-FEB-1998; 98US-0025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI: 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi -
PS Disclosure: Page 58; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXB, BXZXB, BXZXZXB, XBZXZBXB and BXZBXBXZ; and
CC (b) a second peptide template XBZBXBXB and their derivatives selected from
CC the group consisting of XBZBXBX, XBZBXBXB, BXZBXBXB, and
CC XBZBXBXBXZBXB; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.

CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.75;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 12
 |||||:| ||||
 DB 1 ALYKKRNKLK 12

RESULT 11

AA57504
 ID AAY57504 standard; Peptide: 18 AA.

XX AAY57504;

DF 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.

XX Antimicrobial; metapeptide: PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

XX 18-FEB-1998; 98US-0025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

XX Disclosure; Page 59; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBX and its derivatives selected from XBZBXBX, BXZXB, BXZXXB, XBZXXBX and BXZBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXXBX, XBXXBX, BXBXBX, XBZXXB, and XBZXXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;

Best Local Similarity 76.9%; Pred. No. 0.75;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 |||||:| ||||

DB 1 ALYKKRNKLK 13

RESULT 12

AA57468
 ID AAY57468 standard; Peptide: 13 AA.

XX AAY57468;

DF 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-4 SEQ ID NO:6.

XX Antimicrobial; metapeptide: PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

XX 18-FEB-1998; 98US-0025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI: 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

XX Disclosure; Page 108; 16pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBX and its derivatives selected from XBZBXBX, BXZXB, BXZXXB, XBZXXBX and BXZBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXXBX, XBXXBX, BXBXBX, XBZXXB, and XBZXXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 20; Length 13;

Best Local Similarity 69.2%; Pred. No. 0.77;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKRNKLK 13
 |||||:| ||||

DB 1 ARYKRNKLK 13

RESULT 13

AA57467
 ID AAY57467 standard; Peptide: 14 AA.

XX AAY57467;

DF 25-FEB-2000 (first entry)

XX Antimicrobial peptide RP-3 SEQ ID NO:5.
 DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 KM
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 XX
 PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI: 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi
 XX
 PS Disclosure: Page 108; 166pp: English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXBX, BXZXB, BXZXZXB, XBBZXBBX and BBZXBBXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXBX, XBBXXBBX, BXXBBX, XBBZXBB, and
 CC XBBZXBBXXZBBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 CC
 SQ Sequence 14 AA;
 Query Match 69.6%; Score 48; DB 20; Length 14;
 Best Local Similarity 81.8%; Pred. NO. 0.82;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 2 LYKKRNKLLK 12
 DB 2 LYKKRNKLLK 12
 ||:|||||
 RESULT 14
 AAY57466
 ID AAY57466 standard; Peptide: 13 AA.
 XX
 AC AAY57466;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-2 SEQ ID NO:4.
 XX
 KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX

XX 26-AUG-1999.
 PD
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 XX
 PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI: 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi
 XX
 PS Disclosure: Page 107; 166pp: English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXBX, BXZXB, BXZXZXB, XBBZXBBX and BBZXBBXZ; and
 CC (b) a second peptide template XBBXX and their derivatives selected from
 CC the group consisting of XBBXXBX, XBBXXBBX, BXXBBX, XBBZXBB, and
 CC XBBZXBBXXZBBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 CC
 SQ Sequence 13 AA;
 Query Match 68.1%; Score 47; DB 20; Length 13;
 Best Local Similarity 76.9%; Pred. NO. 1.1;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 ALYKKRNKLLKS 13
 DB 1 ARYKKFKKLLKS 13
 ||||:|||||
 RESULT 15
 AAY57503
 ID AAY57503 standard; Peptide: 18 AA.
 XX
 AC AAY57503;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
 XX
 KM Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 XX
 PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 PI Yeaman MR, Shen AJ;
 XX

XX
DR WPI; 1999-527417/44.

XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi
XX

PS Disclosure; Page 59; 166pp; English.

XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXXB and its derivatives
CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBZBXXB and BBZBXXZ; and
CC (b) a second peptide template XBBXX and their derivatives selected from
CC the group consisting of XBBXXB, XBBXXBB, BXBBXB, XBBZXXBB, and
CC XBBZXXBBXZBBX; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
CC sequences used in the exemplification of the present invention.

XX
SQ Sequence 18 AA;

Query Match 68.1%; Score 47; DB 20; Length 18;

Best Local Similarity 76.9%; Pred. No. 1.5;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKKKKKLLKS 13

Db 1 ARYKKKKKKLLKS 13

Search completed: December 30, 2002, 16:22:09
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:13 ; Search time 16 Seconds
(without alignments)
78.109 Million cell updates/sec

Title: US-09-648-816b-9
Perfect score: 69
Sequence: 1 ALYKKWKNKLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*\n1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	71.0	445	2 C71636	probable thiophene
2	44	63.8	827	2 F96647	hypothetical prote
3	43	62.3	445	2 G97846	hypothetical prote
4	42	60.9	245	2 A12126	hypothetical prote
5	42	60.9	397	2 S62579	probable plasma me
6	42	60.9	579	2 B84956	cell division prot
7	41	59.4	286	2 D90609	conserved hypothet
8	41	59.4	531	2 T41151	lysyl-trna synthet
9	40	58.0	87	2 AH1445	hypothetical prote
10	40	58.0	137	1 A36933	diacylglycerol kin
11	40	58.0	170	2 AC3409	dmb protein (limpo
12	40	58.0	175	2 E82941	hypothetical prote
13	40	58.0	361	2 AC1437	glucosamine-fructo
14	40	58.0	453	2 H81151	polya polymerase N
15	39	56.5	119	2 D88013	probable polynucle
16	39	56.5	162	2 A82911	3-isopropylmalate
17	39	56.5	277	2 H86589	glutathione peroxi
18	39	56.5	277	2 H86589	hypothetical prote
19	39	56.5	277	2 H86589	hypothetical prote
20	39	56.5	338	2 T39635	short-chain dehydr
21	39	56.5	342	2 T30368	hypothetical prote
22	39	56.5	439	2 T28196	hypothetical prote
23	39	56.5	487	2 S11886	hypothetical prote
24	39	56.5	492	2 S11885	probable membrane
25	39	56.5	528	4 S11887	hypothetical prote
26	39	56.5	569	2 S11885	glutamate-tRNA lig
27	39	56.5	569	2 E90554	conserved hypothet
28	39	56.5	660	2 S40098	hypothetical prote
29	39	56.5	759	2 T43031	DNA topoisomerase

30	39	56.5	838	2 T40750	hypothetical prote
31	39	56.5	1048	2 S64758	SCD25 protein (ver
32	39	56.5	1250	2 S14177	SCD25 protein (ver
33	38.5	55.8	628	2 AT2333	hypothetical prote
34	38	55.1	117	2 T44090	15150-like transpo
35	38	55.1	118	2 H81143	hypothetical prote
36	38	55.1	180	2 B64353	hypothetical prote
37	38	55.1	185	2 B64394	hypothetical prote
38	38	55.1	293	1 OOCV8V	Bil protein - squa
39	38	55.1	439	2 B6302	hypothetical prote
40	38	55.1	455	2 E71569	lipid A biosynthes
41	38	55.1	520	2 T49478	probable acyltrans
42	38	55.1	520	2 T49478	probable acyltrans
43	38	55.1	896	2 S58360	interleukin-3 rece
44	38	55.1	967	2 S17909	antibiotic Pep5 D
45	38	55.1	969	2 S17909	hypothetical prote

ALIGNMENTS

RESULT 1

C71636 probable thiophene and furan oxidation protein thdf (thdf) RP759 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001

C:Accession: C71636
R.Andersson, S.G.E.; Zomrodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark
Nature 396, 135-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: C71636

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-445 <AMD>

A:Cross-references: GB:AJ235273; GB:AJ235269; MID:93861237; PIDN:CAAL5187.1; PID:9386

A:Experimental source: strain Madrid E

A:Genetics:

A:Gene: thdf; RP759

C:Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu h

C:Keywords: GTP binding; nucleotide binding; P-loop

F:216-332/Domain: translation elongation factor Tu homology <ETU>

F:222-229/Region: nucleotide-binding motif A (P-loop)

F:329-332/Region: GTP-binding NKXD motif

Query Match

Best Local Similarity 71.0%; Score 49; DB 2; Length 445;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LYKKWKNKLK 12

Db 154 LYKKWKNLKLK 164

RESULT 2

F96647 hypothetical protein F19K23.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96647

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96647

A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-827 <STO>
 A:Cross-references: GB:AE005173; NID:g2160138; PIDN:AA60760.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F19K23.6
 A:Map position: 1

Query Match 63.8%; Score 44; DB 2; Length 827;
 Best Local Similarity 61.5%; Pred. No. 26;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKWKNNKLK 13
 ||:|||||
 DB 282 AMKKKMPNLTKS 294

RESULT 3

G97846 hypothetical protein thdf [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: G97846

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
 Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: G97846

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-445 <KUR>

A:Cross-references: GB:AE006914; PIDN:AL03713.1; PID:g15620303; GSPDB:GN00173

C:Genetics:

A:Gene: thdf

C:Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu hom

OY 1 ALYKKWKNNKLK 12
 ||| |::|||
 DB 153 ALYNNMRSQLLK 164

Query Match 62.3%; Score 43; DB 2; Length 445;
 Best Local Similarity 58.3%; Pred. No. 21;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 AI2126 hypothetical protein all2568 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AI2126

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi,
 Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AI2126

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-245 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA74267.1; PID:g17131660; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:
 A:Gene: all2568
 C:Superfamily: Synechocystis hypothetical protein slr1718

Query Match 60.9%; Score 42; DB 2; Length 245;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKWKNNKLK 11
 ||| |::|||
 DB 189 ALYSQWNNLL 199

RESULT 5
 S62579 Probable plasma membrane iron permease - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000

C:Accession: S62579; T38101

R:Murphy, L.; Niblett, D.; Harris, D.
 submitted to the EMBL Data Library, November 1995

A:Reference number: S62573

A:Accession: S62579

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <MUR>

A:Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; PID:g1067209

R:Beck, A.; Reinhardt, R.; Murphy, L.; Niblett, D.; Harris, D.; Barrell, B.G.; Rajand
 submitted to the EMBL Data Library, November 1995

A:Reference number: Z21769

A:Accession: T38101

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-397 <MUR>

A:Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; GSPDB:GN00066; SPDB:S

A:Experimental source: strain 972h-; cosmid clF7

C:Genetics:

A:Gene: SPAC1F7.07c

A:Map position: 1R

C:Superfamily: conserved probable membrane protein YBR207w

OY 2 LYKKWKNNKLK 13
 |::|||:|::|||
 DB 118 LQKKWKNNKLK 129

Query Match 60.9%; Score 42; DB 2; Length 397;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 6
 B64956 cell division protein ftsI [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: B64956

R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp

A:Reference number: A64930; MUID:20445173; PMID:10993077

A:Accession: B64956

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-579 <STO>

A:Cross-references: GB:AP00398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:
 A:Gene: ftsI; BU222
 C:Superfamily: penicillin-binding protein 3

Query Match 60.9%; Score 42; DB 2; Length 579;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LYKKWKNNKLK 13
 :||| ||: |||
 DB 1 MYKKKNNRFLK 12

RESULT 7
 D9609 conserved hypothetical protein MTPU_7800 [imported] - Mycoplasma pulmonis (strain UAB
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C:Accession: D90609
R:Chambrud, I.; Helliou, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulmonis*
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: D90609
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUP>
A:Cross-references: GB:AL445566; PID:G14090195; PIDN:CAC13953.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYP1_7800
A:Genetic code: SGC3

Query Match	59.48%	Score 41	DB 2	Length 286	
Best Local Similarity	54.58%	Score No. 28			
Matches 6	Conservative 4	Mismatches 1	Indels 0	Gaps 0	
Oy	2	LYKKKKKKLLK	12		
		...1111...11			
Db	137	THKTKWNOILK	147		

RESULT 8
T41151
lysyl-trna synthetase - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_rev1599 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T41151
R:Halbert, H.; Duesterhoef, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21973
A:Accession: T41151
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-531 <HML>
A:Cross-references: EMBL:AL031907; PDB:CAA21422.1; GSPDB:GN00068; SPDB:SPCC18.08
A:Experimental source: strain 97zh-; cosmid c18
A:Genetics:
A:Gene: SPDB:SPCC18.08
A:Map position: 3
C:Superfamily: lysine-trna ligase

Query Match	59.4%	Score 41;	DB 2;	Length 531;
Best Local Similarity	50.0%	Pred No. 53;		
Matches	6;	Conservative 4;	Mismatches 2;	Indels 0;
				Gaps 0;
Qy	2	LYKKKNNKLLKS	13	
	:	:::: :: ::		
Db	66	IIKKKNNKIIKITS	77	

RESULT 9
AH1445
hypothetical protein lin0103 [imported] - *Listeria innocua* (strain Cl1p11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH1445
R:Glaser, P.; Fraigneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloekerke, P.; Dominguez-Bernal, L.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madeno, E.; Maitouram, A.; Mok, C.; Schluster, T.; Simoes, N.; Tietze, A.; Vazquez-Roland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:1537279; PMID:11679669
A:Accession: AH1445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 187 <GTA>
A:Cross-references: GB:AL592022; PIDN:CAC9536.1; PID:q16412523; GSPDB:GN00178
A:Experimental source: strain Cl1p11262

```

C:Genetics:
A:Gene: 110103

Query Match      58.0%:  Score 40;  DB 2;  Length 87;
Best Local Similarity 85.7%:
Matches 6;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Oy      3  YKKWKNK 9
        ||||:|
Db      77 YKKWENK 83

```

RESULT 10
A36933
diacylglycerol kinase homolog - Streptococcus mutans
C:Species: Streptococcus mutans
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A36933
R:Yamashita, Y.; Takehara, T.; Kuramitsu, H. K.
J. Bacteriol. 175, 6220-6228, 1993
A:Title: Molecular characterization of a Streptococcus mutans mutant altered in envr
A:Reference number: A36933; MUID:94012483; PMID:8407794
A:Contents: G5S
A:Accession: A36933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <YAM>
A:Note: sequence extracted from NCBI backbone (NCBI:138054, NCBI:P:138056)
C:Superfamily: Bacillus subtilis diacylglycerol kinase dgkA

Query Match	58.0%;	Score 40;	DB 1;	Length 137;
Best Local Similarity	70.0%;	Pred. No. 20;		
Matches	7;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	4	KKWKNNLLKS	13
		:	
Db	13	KKWKNNRTLLTS	22

```

RESULT 11
AC3409
d1nb protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence=revision 01-Feb-2002 #text-change 01-Feb-2002
C:Accession: AC3409
R:DelVecchio, V.G.; Kapatalir, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3352; PMID:11756688
A:Accession: AC3409
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52438.1; PID:g17983242; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1257
A:Map position: 1

```

```

Query Match: 58.0%; Score 40; DB: 2; Length 170;
Best local similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0.

OY 1 ALYKKKKKKLL 11
    | | | | |
Db 9 AYYNQMANKLL 19

```

RESULT 12
E82941
hypothetical protein UN032 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: E82941
 R:Glass, J.J.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 Submitted to GenBank, February 2000
 A:Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a mit
 A:Reference number: A82870
 A:Accession: E82941
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-175 <GLA>
 A:Cross-references: GB:AE002103; GB:AF222894; NID:g6898977; PIDN:AAF30437.1; GSPDB:GN001
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: U0032
 A:Genetic code: SGC3

Query Match 58.0%; Score 40; DB 2; Length 175;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKRNK 9
 :|||
 Db 70 VYKWKMK 77

RESULT 13
 AC1437
 Glucosamine-fructose-6-phosphate aminotransferase (C-terminal domain) homolog lin0034 [1
 C/Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C/Accession: AC1437
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioeche
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Enlitan, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tlherrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A.; Title: Comparative genomics of *Listeria* species
 A:Reference number: AB1077; MUID:21357279; PMID:11679669
 A:Accession: AC1437
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CA095267.1; PID:g16412455; GSPDB:GN00178
 A:Experimental source: strain C11p11262
 C:Genetics:
 A:Gene: lin0034

Query Match 58.0%; Score 40; DB 2; Length 361;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKRNK 9
 :|||
 Db 200 AFYEKKME 208

RESULT 14
 H81151
 polYA polymerase NMB0843 [imported] - *Neisseria meningitidis* (strain MC58 serogroup B)
 C/Species: *Neisseria meningitidis*
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C/Accession: H81151
 R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.R.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qiu, H.; Yamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Ve
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: AB1000; MUID:20175755; PMID:10710307
 A:Accession: H81151
 A>Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-453 <TE>
 A:Cross-references: GB:AE002437; GB:AE002098; NID:g7226072; PIDN:AAF41254.1; PID:g722
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0843

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKRNKMLKS 13
 :|||
 Db 1 MLKKWLNMKLP 12

RESULT 15
 D81870
 Probable polynucleotide adenyllyltransferase (EC 2.7.7.19) NMA1053 [imported] - *Neisse*
 C/Species: *Neisseria meningitidis*
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C/Accession: D81870
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491
 A:Reference number: AB1775; MUID:20222556; PMID:10761919
 A:Accession: D81870
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-453 <PAR>
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84318.1; PID:g737
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: pcnB; NMA1053
 C:Keywords: nucleotidyltransferase

Query Match 58.0%; Score 40; DB 2; Length 453;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKRNKMLKS 13
 :|||
 Db 1 MLKKWLNMKLP 12

Search completed: December 30, 2002, 16:23:26
 Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:28 : Search time 11 Seconds

(without alignments)
49.017 Million cell updates/sec

Title: US-09-648-816b-9
Perfect score: 69
Sequence: 1 ALYKKMKKLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	71.0	445	1 TRME_RICPR	O92C11 rickettsia
2	43	62.3	445	1 TRME_RICCN	O92968 rickettsia
3	42	60.9	245	1 COMB_ANASP	O8Y125 anabaena sp
4	42	60.9	397	1 YAK7_SCHPO	O09919 schizosacch
5	42	60.9	579	1 FTSI_BUCAL	P57317 buchnera ap
6	42	60.9	1971	1 MC3A_MOUSE	O94949 mus musculu
7	40	58.0	137	1 KOGI_STRMU	O06888 streptococc
8	40	58.0	175	1 Y032_UREPA	O92R33 ureaplasma
9	39	55.5	293	1 VBL1_BGMV	P06001 bean golden
10	39	55.5	569	1 SYE_TOBAC	O43794 nicotiana t
11	39	55.5	759	1 TOP3_CAEEL	O61660 caenorhabdi
12	39	56.5	1215	1 BGCN_DROME	O94112 drosophila
13	39	56.5	1253	1 SC25_YEAST	P14771 saccharomyc
14	38	55.1	180	1 Y426_METJA	O51869 methanococc
15	38	55.1	185	1 Y754_METJA	O58164 methanococc
16	38	55.1	252	1 ORC6_HUMAN	O95916 homo sapien
17	38	55.1	262	1 ORC6_MOUSE	O94918 mus musculu
18	38	55.1	293	1 VBL1_SLICV	P21936 squash leaf
19	38	55.1	969	1 DPOM_NEUTN	P33538 neurospora
20	38	55.1	2514	1 POLN_STINDO	P21283 sludbis vir
21	37	53.6	90	1 PLF4_PIG	P30034 sus scrofa
22	37	53.6	130	1 YGH5_YEAST	P33199 saccharomyc
23	37	53.6	249	1 MCT1_CANPA	P21842 canis famli
24	37	53.6	264	1 MEZ4_SCHPO	O94918 mus musculu
25	37	53.6	347	1 Y91_YEAST	P41172 saccharomyc
26	37	53.6	377	1 Y412_MYCGE	P47652 mycoplasma
27	37	53.6	473	1 MWIN_THERMA	O94949 mus musculu
28	37	53.6	645	1 REP_BUCAL	P57654 buchnera ap
29	37	53.6	785	1 PTAL_YEAST	O01329 saccharomyc
30	37	53.6	792	1 SYL_MYCGE	P47508 mycoplasma
31	37	53.6	878	1 IL3B_MOUSE	P26954 mus musculu
32	37	53.6	896	1 CYRB_MOUSE	P26955 mus musculu
33	37	53.6	1068	1 YCF0_MARPO	P12221 marichantia

34	37	53.6	1097	1 KPCL_CANAL	P43057 candida alb
35	37	53.6	3088	1 POLG_PEMVC	O01500 p genome po
36	36.5	52.9	370	1 YG2G_YEAST	P53249 saccharomyc
37	36.5	52.9	500	1 Y1NE_THESJ	O30360 thermoaer
38	36	52.2	83	1 RPOR_SULAC	P39463 sulfobus
39	36	52.2	83	1 Y019_BACAN	O94113 bacterioph
40	36	52.2	137	1 UVSY_BPT4	P04537 bacterioph
41	36	52.2	171	1 VGS56_BPT4	P39262 bacterioph
42	36	52.2	206	1 YMB0_YEAST	O04019 saccharomyc
43	36	52.2	214	1 ST21_RAT	P09005 rattus norv
44	36	52.2	241	1 COMB_SYNY3	P73849 synecocyst
45	36	52.2	247	1 EDIN_STAAU	P24121 staphylococ

ALIGNMENTS

```

RESULT 1
TRME_RICPR
ID TRME_RICPR STANDARD: PRT: 445 AA.
AC O92C11:
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable trna modification GTPase trme.
GN TRME OR THDF OR RP759.
OS Rickettsia prowazekii.
OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales:
OC Rickettsiaceae: Rickettsiidae: Rickettsia.
OX NCBI_Taxid=782;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Madrid E.
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- FUNCTION: EXHIBITS A VERY HIGH INTRINSIC GTPASE HYDROLYSIS RATE.
CC INVOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE 5-
CC METHYLAMINOMETHYL-2-THIOURIDINE, WHICH IS FOUND IN THE WOBBLE
CC POSITION OF SOME TRNAS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
CC PROTEINS. TRME SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ235273; CAA15187.1;
CC InterPro: IPR005289; GTP-binding_dom.
CC InterPro: IPR002917; MMR_HSR1.
CC InterPro: IPR005225; Small-GTP.
CC InterPro: IPR004520; Thdf.
CC Pfam: PF01926; MMR_HSR1.1.
CC TIGRFAMS: TIGR00231; small_gtp.1.
CC TIGRFAMS: TIGR00450; thdf.1.
CC TIGRFAMS: TIGR00650; MG442.1.
KM trna processing; gtp-binding; Complete proteome.
FT NP_BIND 222 229 GTP (POTENTIAL).
FT NP_BIND 269 273 GTP (POTENTIAL).
FT NP_BIND 329 332 GTP (POTENTIAL).
SQ SEQUENCE 445 AA: 49813 MW: 15158F99E716B4F6 CRC64:
Query Match 71.0%: Score 49; DB 1; Length 445;
Best Local Similarity 72.7%: Pred. No. 0.98;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      2 LYKKWKNNKLLK 12
      1111111111
Db      154 LYNNKRNQLLK 164

RESULT 2
TRME_RICCN      STANDARD:      PRT:      445 AA.
ID TRME_RICCN
AC 09ZGB8
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE tRNA modification GTPase trme.
GN TRME OR THDF OR RC1175.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
  Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7.
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
  Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
  Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
  Science 293:2093-2098(2001).
CC -1- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
  Involved in the biosynthesis of the hypermodified nucleoside 5-
  methylaminomethyl-2-thiouridine, which is found in the wobble
  position of some tRNAs (by similarity).
CC -1- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
  PROTEINS. TRME SUBFAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE008665; ALU03713.1;
DR InterPro: IPR005289; GTP-binding_dom.
DR InterPro: IPR002917; MMR_HSR1.
DR InterPro: IPR005225; Small_GTP.
DR InterPro: IPR004520; ThdF.
DR Pfam: PF01926; MMR_HSR1.1.
DR TIGRFAMs: TIGR00650; MG442.1.
DR TIGRFAMs: TIGR00231; small_GTP.1.
DR TIGRFAMs: TIGR00450; thdF.1.
KW tRNA processing; GTP-binding; Complete proteome.
FT NP_BIND 222 229 GTP (POTENTIAL).
FT NP_BIND 269 273 GTP (POTENTIAL).
FT NP_BIND 329 332 GTP (POTENTIAL).
SQ SEQUENCE 445 AA; 49399 MW; 58F4BDE2D1CDAB64 CRC64;

Query Match      62.3%; Score 43; DB 1; Length 445;
Best Local Similarity 58.3%; Pred. NO. 9;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable 2-phosphosulfolactate phosphatase (EC 3.1.3.-).
GN COMB OR ALI2568
OS Anabaena sp. (Strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
  Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
  Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
  Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
CC -1- CATALYTIC ACTIVITY: 2-phosphosulfolactate = sulfolactate +
  phosphate.
CC -1- COFACTOR: Magnesium (by similarity).
CC -1- SIMILARITY: BELONGS TO THE COMB FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AP003589; BAB74267.1;
DR InterPro: IPR005238; 2-ph-phosphatase.
DR TIGRFAMs: TIGR00298; TIGR00298.1.
KW Hydrolyase; Magnesium; Complete proteome.
SQ SEQUENCE 245 AA; 26694 MW; BC7F4BBAE5B6958 CRC64;

Query Match      60.9%; Score 42; DB 1; Length 245;
Best Local Similarity 63.6%; Pred. NO. 7.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      1 ALYKKWKNNKLL 11
      1111111111
Db      189 ALYSQWQNNLL 199

RESULT 4
YAK7_SCHPO      STANDARD:      PRT:      397 AA.
AC 009919;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ClF7.07c in chromosome I.
GN SPAC1F7.07c.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
  Schizosaccharomycetales; Schizosaccharomycetaceae;
  Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
  Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
  Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
  Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G.,
  Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
  James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
  Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

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RA Skelton J., Stimmings M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE FTPL FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z67998; CAA91954.1; -
 DR InterPro: IPR004923; FTPL.
 DR Pfam: PF03239; FTPL1.1.
 DR Hypothetical protein; Transmembrane.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 SQ SEQUENCE 397 AA: 44314 MW: 1D98E41AD1FD708F CRC64:
 Query Match 60.9%; Score 42; DB 1; Length 397;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKMKRKLKLS 13
 Db 118 LDEKKMKRLKLS 129
 RESULT 5
 FTSI_BUCAI
 ID FTSI_BUCAI STANDARD: PRT: 579 AA.
 AC P57317.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptidoglycan synthetase ftsi (Penicillin-binding protein 3) (PBP-3).
 GN FTSI OR B0222.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1996;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RL Buchnera sp. Aps.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CELL WALL FORMATION. ESSENTIAL FOR THE FORMATION OF A
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES OF CROSS-LINKED
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES (BY SIMILARITY).
 CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- DOMAIN: HAS AN N-TERMINAL PENICILLIN INSENSITIVE TRANSGLYCOSYLASE

CC DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) & A CARBOXY-TERMINAL
 CC PENICILLIN-SENSITIVE TRANSEPTIDASE DOMAIN (CROSS-LINKING OF THE
 CC PEPTIDE SUBUNITS)
 CC -1- SIMILARITY: BELONGS TO THE TRANSEPTIDASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AP001118; BAB12938.1; -
 DR InterPro: IPR005311; pnp_dimer.
 DR InterPro: IPR001460; Transpeptidase.
 DR Pfam: PF00905; Transpeptidase; 1.
 DR Pfam: PF03717; PBP_dimer; 1.
 KW Transmembrane; Peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome.
 FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT_SITE 305 305 ACYLATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA: 65204 MW: E3717820808CAD12 CRC64:
 Query Match 60.9%; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKMKRKLKLS 13
 Db 1 MYKKKKNRFLKS 12
 RESULT 6
 MCM3A_MOUSE
 ID MCM3A_MOUSE STANDARD: PRT: 1971 AA.
 AC O9WU9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 80 kDa MCM3-associated protein (GAMP protein).
 GN MCM3AP OR GAMP OR MAP80.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C X NZB;
 RX MEDLINE=20197882; PubMed=10733502;
 RA Kuwahara K., Yoshida M., Kondo E., Sakata A., Watanabe Y., Abe E.,
 RA Kouno Y., Tomiyasu S., Fujimura S., Tokuhisa T., Kimura H., Ezaki T.,
 RA Sakaguchi N.;
 RT "A novel nuclear phosphoprotein, GAMP, is up-regulated in centrocytes
 RT of the germinal center and associated with MCM3, a protein essential
 RT for DNA replication.";
 RL Blood 95:2321-2328(2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE NUCLEAR LOCALIZATION PATHWAY OF
 CC MCM3 (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH MCM3.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE SAC3 FAMILY.
 CC -----
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 CC -----

CC -----
 DR EMBL: AJ006590: CAB4241.1; -
 DR MGD: MGI:1930089: Mgm3ap.
 DR InterPro: IPR005062: SAC3_GANP.
 DR Pfam: PF03399: SAC3_GANP; 1.
 DR Nuclear protein; Phosphorylation.
 SO SEQUENCE 1971 AA; 217138 MW; 5F342E256C007E24 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 1971;
 Best Local Similarity 77.8%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKKWKMKLL 11
 1:|||||1
 Db 1710 YKKWKMKSL 1718

RESULT 7
 KDGL_STRMU STANDARD; PRT; 137 AA.

AC Q05888: 051807; (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Diacylglycerol kinase (EC 2.7.1.107) (DAGK) (Diglyceride kinase)
 DE (DCK).
 GN DCKA OR DCK.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS-5;
 RX MEDLINE=94012483; PubMed=8407794;
 RA Yamashita Y., Takehara T., Kuramitsu H.K.;
 RT "Molecular characterization of a Streptococcus mutans mutant altered
 in environmental stress responses.";
 RL J. Bacteriol. 175:6220-6228(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T8;
 RX MEDLINE=98083071; PubMed=9422608;
 RA Chen P., Novak J., Qi F.-Q., Caulfield P.W.;
 RT "Diacylglycerol kinase is involved in regulation of expression of the
 lactobiotic mutacin II of Streptococcus mutans.";
 RL J. Bacteriol. 180:167-170(1998).
 CC -I- FUNCTION: RECYCLING OF DIACYLGLYCEROL PRODUCED DURING THE
 TURNOVER OF MEMBRANE PHOSPHOLIPID. MAY PLAY A ROLE IN ADAPTABILITY
 TO ENVIRONMENTAL STRESS CONDITIONS SUCH AS ACID TOLERANCE,
 ELEVATED TEMPERATURES AND HIGH OSMOLARITY.
 CC -I- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
 diacylglycerol 3-phosphate.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -I- SIMILARITY: BELONGS TO THE BACTERIAL DIACYLGLYCEROL KINASE FAMILY.
 CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
 CC -----
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 CC -----
 CC EMBL: LI2211; AAA26867.1; -
 DR EMBL: AF000954; AAC38047.1; -
 DR InterPro: IPR000829; DAGK_prokar.
 DR Pfam: PF01219; DAGK_prokar; 1.
 DR Prodom: PD010722; DAGK_prokar; 1.
 DR PROSITE: PS01069; DAGK_PROKAR; 1.
 KW Phospholipid biosynthesis; Transferase; Kinase; Transmembrane.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 43 58 POTENTIAL.
 FT TRANSMEM 62 78 POTENTIAL.
 FT DOMAIN 79 108 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 109 129 POTENTIAL.
 FT CONFLICT 128 129 LT -> VP (IN REF. 2).
 SO SEQUENCE 137 AA; 15380 MW; 4F01654885319125 CRC64;

Query Match 58.0%; Score 40; DB 1; Length 137;
 Best Local Similarity 70.0%; Pred. No. 9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKKKKLKS 13
 1:||||1
 Db 13 KKKKKRLTS 22

RESULT 8
 Y032_UREPA STANDARD; PRT; 175 AA.

AC Q9PRB3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein U0032.
 GN U0032.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sevovar 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Helner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 urealyticum.";
 RL Nature 407:757-762(2000).
 CC -----
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 CC -----
 CC EMBL: AE002103; AAF30437.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 175 AA; 20950 MW; 93FDA028712E5222 CRC64;

Query Match 58.0%; Score 40; DB 1; Length 175;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNK 9
 1:||||1
 Db 70 YKKWKMK 77

RESULT 9
 VBL1_BGMV STANDARD; PRT; 293 AA.

AC P06001;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE B11 protein (33.1 kDa protein).
 GN BCL1.
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; GeminiViridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 RL regulation in geminiviruses";
 CC Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES BL1 PROTEIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M10080; AAA46323.1; -;
 DR InterPro: IPR000211; Gemini.B1.
 DR Pfam: PF00845; Gemini.B1; 1
 SO SEQUENCE 293 AA; 33099 MW; CC3C4E0E93A79441 CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 293;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKKKKKLKS 13
 Db 178 YKKKKKKLKS 188

RESULT 10
 SVE_TOBAC
 ID SVE_TOBAC STANDARD; PRT; 569 AA.
 AC Q43794;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GLURS)
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. SRL; TISSUE=leaf;
 RA Andersen R.V.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X83524; CA58506.1; -;
 DR HSSP: P27000; 1GLN.
 DR InterPro: IPR004527; GltX_bact.
 DR InterPro: IPR000924; Glt_LRNA_synth_1c.
 DR InterPro: IPR001412; tRNA-synt_1c.
 DR Pfam: PF00748; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTGLU.
 DR TIGRFAMs: TIGR00464; gltX_bact. 1.
 DR PROSITE: PS00178; AA.TRNA.LIGASE.I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SITE 62 72 "HIGH" REGION.
 FT SITE 303 307 "KMSK" REGION.
 FT BINDING 306 306 ATP (BY SIMILARITY).
 SO SEQUENCE 569 AA; 63338 MW; F2E81D73460A1844 CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 569;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKKKLKS 13
 Db 141 ALYKKKKLKS 153

RESULT 11
 TOP3_CAEFL
 ID TOP3_CAEFL STANDARD; PRT; 759 AA.
 AC Q6160; Q90223;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA topoisomerase III (EC 5.99.1.2).
 GN TOP-3 OR Y56A3A.27.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kim Y.-C., Koo H.-S.;
 RT "cDNA cloning and overexpression of Caenorhabditis elegans DNA
 RT topoisomerase III.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Matthews L.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF057032; AAC13567.1; -;
 DR EMBL: AL132860; CAB60518.2; -;
 DR Wormpep: Y56A3A.27; CE28138.
 DR InterPro: IPR002936; DNAPrim_toprim.
 DR InterPro: IPR003602; DNATopI_ATP_bind.
 DR InterPro: IPR003602; DNATopI_DNA_bind.
 DR InterPro: IPR000380; ProK_topoisomase.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01751; Topoisom_1.
 DR PRINTS: PR00417; PRTISMASE1.
 DR SMART: SM00437; TOP1AC; 1.
 DR SMART: SM00436; TOP1BC; 1.
 DR SMART: SM00493; TOP1RM; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA-binding.
 FT ACT SITE 334 334 DNA CLEAVAGE (BY SIMILARITY).
 SO SEQUENCE 759 AA; 85438 MW; 3D862412D72946BD CRC64;

Query Match
 Best Local Similarity 56.5%; Score 39; DB 1; Length 759;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKMKKML 11
 :|||:|
 Db 455 LYKMKGNRL 464

RESULT 12
 BGCN.DROME STANDARD: PRT: 1215 AA.
 ID BGCN.DROME 09M113:
 AC 09M113: 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Benign gonial cell neoplasm protein.
 GN BGCN OR B(2)GCN OR CG30170/CG10331.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 OX NCBI_TaxID=7227;
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=20384590; PubMed=10924476;
 RX Chlstein B., Lavoe C.A., Vef O., Gateff E., McKearn D.M.;
 RT "The Drosophila cytoskeleton differentiation factor, benign gonial cell
 RT neoplasm, is related to DEXH-box proteins and interacts genetically
 RT with bag-of-marbles."
 RL Genetics 155:1809-1819(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Anil J.F., Agbayani A., An H.-J., Andrews-Prankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bess P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jaitani B., Kalush F., Karpen G.H., Ke Z., Kienison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS.

RC STRAIN=Berkley;
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Celniker S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman J.P., Carlson J.W., Celniker S.E.,
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Seale S.M.J., Smith E., Shu S., Smutnack F.,
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome."
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ESSENTIAL CYSTOBLAST DIFFERENTIATION FACTOR REQUIRED FOR
 CC BAM FUNCTION IN ASYMMETRIC DIVISION OF THE GERMLINE STEM CELLS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND IN 5-8 GERMLINE STEM
 CC CELLS OF OVARIES. IMMEDIATELY ADJACENT TO TERMINAL FILAMENT.
 CC -1- SIMILARITY: SOME SIMILARITIES TO DEXH-BOX PROTEINS BUT OUTSIDE OF
 CC THE HELICASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 ANK REPEAT.
 CC -----
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 CC -----
 CC DR EMBL: AF255662; AAF91348.1; -
 CC DR EMBL: AF003462; AAF47077.2; -
 CC DR Flybase: FBgn004581; dgcN.
 CC DR InterPro: IPR002110; ANK.
 CC DR Pfam: PF00023; ank; 2.
 CC DR SMART: SM00248; ANK; 1.
 CC DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC DR PROSITE: PS50088; ANK_REPEAT; 1.
 CC KW Developmental protein; ANK repeat.
 CC FT REPEAT 407 439
 CC FT SEQUENCE 1215 AA; 139278 MW; 11F83C1B3816F2CD CRC64;
 SQ

Query Match 56.5%; Score 39; DB 1; Length 1215;
 Best Local Similarity 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKMKKML 10
 :|||:|
 Db 792 LYKMKGNRM 800

RESULT 13
 SC25.YEAST STANDARD: PRT: 1253 AA.
 ID SC25.YEAST 01APR-1990 (Rel. 14, Created)
 AC P14771:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SCD25 protein.
 GN SCD25 OR SDC25 OR YIL016W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M303;
 RX MEDLINE=91094833; PubMed=1986220;
 RA Damek F., Boy-Marcotte F., le Roscouet D., Guilbaud R., Jacquet M.;
 RT "SCD25, a CDC25-like gene which contains a RAS-activating domain and
 RT is a dispensable gene of Saccharomyces cerevisiae."
 RL Mol. Cell. Biol. 11:202-212(1991).
 RN [2]
 RP SEQUENCE OF 668-1253 FROM N.A.
 RC STRAIN=01136;
 RX MEDLINE=89306677; PubMed=2545538;

RA Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.;
 RT "The C-terminal part of a gene partially homologous to CDC 25 gene
 suppresses the cdc25-5 mutation in *Saccharomyces cerevisiae*."; *Gene*
 77:21-30(1989).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=90260633; PubMed=2188363;
 RA Crechet J.B., Poulet P., Mistou M.-Y., Parmegiani A., Camonis J.,
 RA Boy-Marcotte E., Damak F., Jacquet M.;
 RT "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-
 terminal domain of SCD25."; *Science* 248:866-868(1990).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=91156312; PubMed=2000228;
 RA Rey I., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
 RA Guilhaud R., Jacquet M., Tocque B.;
 RT "The COOH-domain of the product of the *Saccharomyces cerevisiae* SCD25
 gene elicits activation of p21-ras proteins in mammalian cells."; *Oncogene*
 6:347-349(1991).
 RL CC -1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
 CC -1- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES
 CC CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
 CC -1- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL: M2647; AAA16565.1; -
 DR PIR: S14177; S14177.
 DR SGD: S0003939; SDC25.
 DR InterPro: IPR001895; RasGEF_N.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00617; RasGEF; 1.
 DR Pfam: PF00618; RasGEF; 1.
 DR SMART: SM00147; RasGEF; 1.
 DR SMART: SM00229; RasGEF; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR PROSITE: PS0002; SH3; 1.
 DR KW Guanine-nucleotide releasing factor; Cell cycle; Cell division;
 KM SH3 domain.
 FT DOMAIN 26 98 SH3.
 FT DOMAIN 74 79 POLY-ASN.
 FT DOMAIN 434 437 POLY-ARG.
 FT VARIANT 584 590 DVVVKFI -> V (IN STRAIN 01136).
 SQ SEQUENCE 1253 AA; 144979 MW; 2DE2C9C21E3E60D CRC64;
 Query Match 56.5%; Score 39; DB 1; Length 1253;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LYKKRNKLKLS 13
 DB 978 LQIKRNKNTKS 989
 RESULT 14
 Y426_METJA STANDARD; PRT; 180 AA.
 AC 057869;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0426.

GN M0426.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*."; *Science* 273:1058-1073(1996).
 RL CC -----
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 CC -----
 DR EMBL: U67494; AAB98419.1; -
 DR TIGR: M0426; -
 DR KW Hypothetical protein; Complete proteome.
 FT DOMAIN 45 51 POLY-GLU.
 SQ SEQUENCE 180 AA; 21609 MW; E9BE603DEBAE4053 CRC64;
 Query Match 55.1%; Score 38; DB 1; Length 180;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKKRNK 9
 DB 101 ALYIDMKRN 109
 RESULT 15
 Y754_METJA STANDARD; PRT; 185 AA.
 AC Q58164;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0754.
 GN M0754.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*."; *Science* 273:1058-1073(1996).
 RL CC -----

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DR EMBL: D67521; AAB98756.1; -;
 DR TIGR: M70754; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 185 AA; 21765 MW; 2CE5EC9D424895F6 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 185;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKMLKS 13
 DB 38 LYKKWKMLQIFKN 49

Search completed: December 30, 2002, 16:22:28
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:20:53 ; Search time 28 seconds
(without alignments)
95.665 Million cell updates/sec

Title: US-09-648-816b-9
Perfect score: 69
Sequence: 1 ALYKKMKKLKLS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTRMBL_21:*\n2: sp_archaea:*\n3: sp_bacteria:*\n4: sp_fungi:*\n5: sp_human:*\n6: sp_invertebrate:*\n7: sp_mhc:*\n8: sp_mammal:*\n9: sp_organelle:*\n10: sp_phage:*\n11: sp_plant:*\n12: sp_virus:*\n13: sp_vertebrate:*\n14: sp_unclassified:*\n15: sp_virus:*\n16: sp_bacteriap:*\n17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	68.1	508	16	Q8R6X0 thermomac
2	44	63.8	215	2	Q9Z655 zymomonas m
3	44	63.8	827	10	004578 arabidopsis
4	43	62.3	1891	12	Q8Q024 arabidopsis
5	43	62.3	2508	12	Q8Q023 arabidopsis
6	42	60.9	293	12	Q67584 bean golden
7	41	59.4	107	10	Q9L196 arabidopsis
8	41	59.4	286	16	Q98PE3 arabidopsis
9	41	59.4	307	2	Q9KH70 mycoplasma
10	41	59.4	439	12	Q8V3P3 swinepox vi
11	41	59.4	531	3	074858 schizosacch
12	41	59.4	762	8	Q9G872 rhodomonas
13	40	58.0	87	16	Q92FK1 listeria in
14	40	58.0	170	16	Q8YGA3 brucella me
15	40	58.0	259	2	P72185 propionibac
16	40	58.0	361	16	Q92FR9 listeria in

17	40	58.0	362	16	Q981G4 rhizobium l
18	40	58.0	453	16	Q9JZY9 neisseria m
19	40	58.0	435	16	Q9JY08 neisseria m
20	40	58.0	506	10	Q9SKW7 zea mays (m
21	40	58.0	570	10	Q9PEA2 arabidopsis
22	40	58.0	570	10	Q940P6 arabidopsis
23	40	58.0	627	10	Q9MA10 arabidopsis
24	40	58.0	976	2	054222 staphylococ
25	40	58.0	1723	5	Q8WRD0 plasmodium
26	39	56.5	162	16	Q9P0K0 ureaplasma
27	39	56.5	230	16	Q9EW10 streptomyces
28	39	56.5	277	16	Q9Z7B2 chlamydia p
29	39	56.5	293	12	Q67573 bean golden
30	39	56.5	338	3	074732 schizosacch
31	39	56.5	439	12	Q9YWS7 melanoplus
32	39	56.5	446	16	Q926P3 listeria in
33	39	56.5	487	3	Q05377 saccharomyc
34	39	56.5	492	3	Q12317 saccharomyc
35	39	56.5	499	10	Q9SWE3 saccharomyc
36	39	56.5	528	3	Q05378 nicotiana t
37	39	56.5	569	16	Q98OM0 clostridium
38	39	56.5	660	2	Q45923 clostridium
39	39	56.5	694	5	Q8T4D2 dirosophila
40	39	56.5	770	5	Q9VNT2 dirosophila
41	39	56.5	840	3	Q13652 schizosacch
42	39	56.5	879	5	Q9GUJ9 leishmania
43	39	56.5	1012	5	Q97035 hydra magni
44	39	56.5	1048	3	Q12037 saccharomyc
45	39	56.5	1169	5	Q9N1S0 toxoplasma

ALIGNMENTS

RESULT 1
ID Q8R6X0 PRELIMINARY; PRT; 508 AA.
AC Q8R6X0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE2663.
GN TTE2663.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013206; AAM25782.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 508 AA; 58270 MW; BCBB364EB79D845 CRC64;
QY 2 LYKKMKKLKLS 13
Db 310 LYKKMKKLKLS 321
Query Match 68.1%; Score 47; DB 16; Length 508;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RESULT 2
Q9Z655 PRELIMINARY; PRT; 215 AA.
AC Q9Z655;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Hypothetical 25.2 kDa protein.
 OS Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 OX NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ZM4;
 RA Um H.W., Kang H.S.;
 RT "Sequence analysis of 4349 fosmid clone of Zymomonas mobilis ZM4.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF102543; AAD19422.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 215 AA; 25210 MW; 48D308672D9A05B CRC64;

Query Match 63.8%; Score 44; DB 2; Length 215;
 Best Local Similarity 72.7%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ALYKKWKRLK 12
 Db 36 LFKSKAKLKLK 46

RESULT 3
 ID 004578 PRELIMINARY; PRT; 827 AA.
 AC 004578;

DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE F19K23.6 protein.
 GN F19K23.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids; II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Osborne B.I., Vysotskaia V.S., Toriumi M., Yu G., Oji O., Shen Y.K.,
 RA Arango R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
 RA Feng J., Kim C., Kurtz D., Li Y., Shin P., Sun H., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC000375; AAB60760.1; -
 DR InterPro: IPR003690; mTERF.
 DR InterPro: IPR003880; Pplantn_attach.
 DR Pfam: PF02536; mTERF. 2.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
 SQ SEQUENCE 827 AA; 92517 MW; 0D53CB85234555B CRC64;

Query Match 63.8%; Score 44; DB 10; Length 827;
 Best Local Similarity 61.5%; Pred. No. 70;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKWKRLK 13
 Db 282 AMFKKWNILTKS 294

RESULT 4
 080024

ID 080024 PRELIMINARY; PRT; 1891 AA.
 AC 080024;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Nonstructural polyprotein 123.
 OS Sindbis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX NCBI_TaxID=11034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MRE16;
 RA Myles K.M., Pietro D.J., Olson K.E.;
 RT "Virus produced from a full-length, molecular clone of the Malaysian
 Sindbis virus, MRE16, efficiently infects Aedes aegypti and Culex
 tritaeniorhynchus by the oral route.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492770; AAM10975.1; -
 KW Polyprotein.
 FT CHAIN 1 540 NSP1.
 FT CHAIN 541 1347 NSP2.
 FT CHAIN 1348 1891 NSP3.
 SQ SEQUENCE 1891 AA; 210105 MW; 07ED7460B7FBBC0 CRC64;

Query Match 62.3%; Score 43; DB 12; Length 1891;
 Best Local Similarity 53.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKKWKRLK 13
 Db 1383 ALYKKWPNFVDS 1395

RESULT 5
 ID 080023 PRELIMINARY; PRT; 2508 AA.
 AC 080023;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Nonstructural polyprotein 1234 (Fragment).
 OS Sindbis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX NCBI_TaxID=11034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MRE16;
 RA Myles K.M., Pietro D.J., Olson K.E.;
 RT "Virus produced from a full-length, molecular clone of the Malaysian
 Sindbis virus, MRE16, efficiently infects Aedes aegypti and Culex
 tritaeniorhynchus by the oral route.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF492770; AAM10974.1; -
 KW Polyprotein.
 FT CHAIN 1 >540 NSP1.
 FT CHAIN 541 >1347 NSP2.
 FT CHAIN 1348 >1898 NSP3.
 FT CHAIN 1899 >2506 NSP4.
 FT NON_TER 2508 2508
 SQ SEQUENCE 2508 AA; 279395 MW; D3F55794FABF740 CRC64;

Query Match 62.3%; Score 43; DB 12; Length 2508;
 Best Local Similarity 53.8%; Pred. No. 3e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKKWKRLK 13
 Db 1383 ALYKKWPNFVDS 1395

RESULT 6

067584
ID 067584 PRELIMINARY: PRT: 293 AA.
AC 067584;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN BL1 protein.
GN
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
geminiviruses and determining their infectivity by electric discharge
particle acceleration."
RT phytopathology 81:980-985(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hideyat S.H., Martinez R.T., Leong S.A., Faria J.C.,
Morales F.J., Maxwell D.P.;
RT "Differentiation of bean-infecting geminiviruses by nucleic acid
hybridization probes and aspects of bean golden mosaic in Brazil."
RT Plant Dis. 75:336-342(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RT "Genetic diversity in geminiviruses causing bean golden mosaic
disease: The nucleotide sequence of the infectious cloned DNA
components of a Brazilian isolate of bean golden mosaic geminivirus."
RT Submitted (May-1992) to the EMBL/GenBank/DBJ databases.
RL EMBL: M88687; AAA46317.1; -
DR InterPro: IPR000211; GeminL.B1.
DR Pfam: PF00845; GeminL.B1: 1.
SQ SEQUENCE 293 AA: 33049 MW: FER2D535B3984854 CRC64;

Query Match 60.9%; Score 42; DB 12; Length 293;
Best Local Similarity 63.6%; Pred. No. 54;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKKNKLK 13
Db 178 YGKWKRLK 188

RESULT 7
09L196 PRELIMINARY: PRT: 107 AA.
ID 09L196
AC 09L196;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Genomic DNA, chromosome 3, pl clone:IM010.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=20363099; PubMed=10907853;
RX Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
TAC and BAC clones.";

RL DNA Res. 7:217-221(2000).
DR EMBL: AP001309; BAB02593.1; -
SQ SEQUENCE 107 AA: 12145 MW: 020DD058429B14BC CRC64;

Query Match 59.4%; Score 41; DB 10; Length 107;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKKNKL 11
Db 96 HKWKKNKV 104

RESULT 8
098PE3 PRELIMINARY: PRT: 286 AA.
ID 098PE3
AC 098PE3;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein MYPU_7800.
GN MYPU_7800.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chumbud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL: AL445565; CAC13953.1; -
DR MYPULIST; MYPU_7800; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA: 34833 MW: 17BAE37548A9C081 CRC64;

Query Match 59.4%; Score 41; DB 16; Length 286;
Best Local Similarity 54.5%; Pred. No. 76;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKKNKLK 12
Db 137 IHKWKKNOLK 147

RESULT 9
09KH70 PRELIMINARY: PRT: 307 AA.
ID 09KH70
AC 09KH70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Thermostable dipeptidase Bdp.
GN BDP.
OS Brevibacillus borstelensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Penibacillaceae; Brevibacillus.
OX NCBI_TaxID=45462;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCS-1;
RA Kwon S., Hong S., Sung M.;
RT "A Novel Thermostable Dipeptidase from Brevibacillus borstelensis BCS-
1.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP268876; AAP97793.1; -
DR InterPro: IPR000180; Renal_dipeptidase.
DR Pfam: PF01244; Renal_dipeptidase; 1.

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SQ SEQUENCE 307 AA: 34975 MW: 502FCC83754E20E2 CRC64;
Query Match
Best Local Similarity 59.4%; Score 41; DB 2; Length 307;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKMK 9
    |||||
Db 10 ALYKKMK 18

RESULT 10
Q8V3P3 PRELIMINARY; PRT; 439 AA.
ID Q8V3P3
AC Q8V3P3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE SPV051 hypothetical protein.
GN SPV051.
OS Swinepox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
OX NCBL_TaxID=10276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17077-99;
RX MEDLINE=21624277; PubMed=1152168;
RA Alonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
RA Kutish G.F., Rock D.L.;
RT "The genome of swinepox virus."
RL J Virol. 76:783-790(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=17077-99;
RA Alonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
RA Kutish G.F., Rock D.L.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF410153; AAL69790.1; -.
KW Hypothetical protein.
SQ SEQUENCE 439 AA: 50984 MW: 4991293795BF3850 CRC64;

Query Match
Best Local Similarity 59.4%; Score 41; DB 12; Length 439;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKKMK 7
    |||||
Db 325 ALYKKMK 331

RESULT 11
Q74858 PRELIMINARY; PRT; 531 AA.
ID Q74858
AC Q74858;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Lysyl-tRNA synthetase.
GN SPC18.08.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBL_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA (AMINO ACID) = AMP +
CC DIPHOSPHATE + L-AMINOACYL-TRNA (AMINO ACID).
CC -I- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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DR EMBL: AL031907; CAA21422.1; -.
DR HSSP; P14825; 1c10.
DR InterPro: IPR002106; AATRNA_LigaseII.
DR InterPro: IPR004364; tRNA-synt_2.
DR InterPro: IPR002313; tRNA-synt_lys_2.
DR InterPro: IPR004365; tRNA-anti.
DR Pfam: PF00152; tRNA-synt_2; 1.
DR Pfam: PF01336; tRNA-anti; 1.
DR PRINTS; PR00982; TRNASYNTHLYS.
DR TIGRFAMs; TIGR00499; lysS_bact; 1.
DR PROSITE; PS00179; AA-TRNA-LIGASE-II_1; 1.
DR PROSITE; PS00339; AA-TRNA-LIGASE-II_2; UNKNOWN_1.
KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ SEQUENCE 531 AA: 60285 MW: AA8418CDF32C416F CRC64;

Query Match
Best Local Similarity 59.4%; Score 41; DB 3; Length 531;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKMKKLKS 13
    :||:|:|:|
Db 66 ILEKMKKTKTS 77

RESULT 12
Q9G8T2 PRELIMINARY; PRT; 762 AA.
ID Q9G8T2
AC Q9G8T2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Orf762.
GN Orf762.
OS Rhodomonas salina.
OC Mitochondrion.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBL_TaxID=52970;
RN [1]
RP SEQUENCE FROM N.A.
RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
RT "Algae with secondary chloroplasts have mitochondria that originate
RT from the host."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF288090; AAG17765.1; -.
DR InterPro: IPR000442; Intron_maturase2.
DR InterPro: IPR000477; RYase.
DR Pfam: PF01348; Intron_maturase2; 1.
DR Pfam: PF00078; rvt; 1.
KW Mitochondrion; RNA-directed DNA polymerase.
SQ SEQUENCE 762 AA: 87494 MW: 9235F3F7EDB04911 CRC64;

Query Match
Best Local Similarity 59.4%; Score 41; DB 8; Length 762;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKMKKLKS 13
    |:|:|:|
Db 674 KKKMKKLKS 683

RESULT 13
Q92FK1 PRELIMINARY; PRT; 87 AA.
ID Q92FK1
AC Q92FK1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein lin0103.
GN LIN0103.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBL_TaxID=1642;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CLIP 11262 / SEROVAR 6A;
 RX PubMed-11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charid A., Chetoui F., Couve E., de Darivar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fishi H., Garcia-del Portillo F., Garido P.,
 Gantier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
 Madueno E., Maicounam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluteler T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001).
 DR EMBL: AL596163; CAC95336.1; -
 DR Listlist: LIN00103; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 87 AA; 10135 MW; E1A37A29CACE4DF CRC64;

Query Match 58.0%; Score 40; DB 16; Length 87;
 Best Local Similarity 85.7%; Pred. NO. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YKKWKNK 9
 DB 77 YKKWKNK 83

RESULT 14
 ID 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE D1NB protein.
 GN BMEI1257.
 OS *Brucella melitensis*.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed-11756688;
 RA DelVecchio V.G., Kaputal V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.,
 RT "The genome sequence of the facultative intracellular pathogen
 RT *Brucella melitensis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009564; AAL52438.1; -
 KW Complete proteome.
 SQ SEQUENCE 170 AA; 19976 MW; 448E7185D7860B66 CRC64;

Query Match 58.0%; Score 40; DB 16; Length 170;
 Best Local Similarity 63.6%; Pred. NO. 66;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLL 11
 DB 9 AYYNOMANKLL 19

RESULT 15
 ID P72185 PRELIMINARY; PRT; 259 AA.
 AC P72185;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Repressor protein (HEMR protein).
 GN HEHR.
 OS *Propionibacterium freudenreichii*.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
 OC Propionibacterium.
 OX NCBI_TaxID=1744;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roessner C.A.;
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RX MEDLINE=93175878; PubMed=8439165;
 RA Murakami K., Hashimoto Y., Murooka Y.,
 RT "Cloning and characterization of the gene encoding glutamate 1-
 RT semialdehyde 2,1-aminomutase, which is involved in delta-
 RT aminolevulinic acid synthesis in *Propionibacterium freudenreichii*.";
 RL Appl. Environ. Microbiol. 59:347-350(1993).
 RN [3]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RA Hashimoto Y., Yamashita Y., Ono H., Murooka Y.,
 RL J. Ferment. Bioeng. 82:93-100(1996).
 RN [4]
 RP SEQUENCE OF 17-259 FROM N.A.
 RC STRAIN-IF012424;
 RX MEDLINE=97306686; PubMed=9163953;
 RA Hashimoto Y., Yamashita Y., Murooka Y.,
 RT "The *Propionibacterium freudenreichii* hemYBXR gene cluster, which
 RT encodes enzymes and a regulator involved in the biosynthetic pathway
 RT from glutamate to protoheme.";
 RL Appl. Microbiol. Biotechnol. 47:385-392(1997).
 CC -i- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: U51164; AAB07865.1; -
 DR EMBL: D85417; BAA21913.1; -
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; tetr. 1.
 KW DNA-binding; Transcription regulation.
 SQ SEQUENCE 259 AA; 27426 MW; 5FCB0EFF342606170 CRC64;

Query Match 58.0%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. NO. 99;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKWKNK 9
 DB 76 ALYKKWKNK 84

Search completed: December 30, 2002, 16:23:05
 Job time : 31 secs

